(b) a complement of the nucleotide sequence, wherein the complement and the nucleotide sequence consist of the same number of nucleotides and are 100% complementary.

5. (Amended) The polynucleotide of Claim 1 wherein the polynucleotide encodes a polypeptide selected from the group consisting of SEQ ID NOs:4, 12, and 16.

6. (Amended) The polynucleotide of Claim 1 wherein the polynucleotide comprises a nucleotide sequence selected from the group consisting of SEQ ID NO: 3, 11, and 15.

24. (Amended) A recombinant DNA construct comprising the polynucleotide of Claim 1 operably linked to at least one regulatory sequence.

25. (Amended) A method for altering the level of pathogen resistance in a plant, the method comprising the steps of:

(a) transforming a plant cell with the recombinant DNA construct of Claim 24;

(b) culturing the transformed plant cell under conditions suitable for the expression of the polynucleotide;

(c) maintaining the plant cell under conditions that are suitable for its development into a plant; and

(d) comparing the level of pathogen resistance of the plant cell containing the polynucleotide and a plant cell not containing the polynucleotide.

Please add the following claims 26-32:

26. (new) A vector comprising the polynucleotide of Claim 1.

27. (new) A cell comprising the recombinant DNA construct of Claim 24.

28. (new) The cell of Claim 27, wherein the cell is selected from the group consisting of a yeast cell, a bacterial cell and a plant cell.

29. (new) A virus comprising the recombinant DNA construct of Claim 24.

30. (new) A transgenic plant comprising the recombinant DNA construct of Claim 24.

31. (new) A method for transforming a cell, comprising introducing into a cell recombinant DNA construct of Claim 24.

32. (new) A method for producing a transgenic plant comprising

(a) transforming a plant cell with recombinant DNA construct of Claim 24, and

(b) regenerating a plant from the transformed plant cell.

REMARKS

Claims 1-6 and 24-32 are now pending, with claim 1 being the sole independent claim.

Claims 7-23 have been canceled without prejudice to or disclaimer of the subject matter recited therein. Claims 1, 5-6, and 24-25 have been amended, and Claims 26-32 have been added. The specification has been amended to correct typographical errors. No new matter is believed to have been added.

RESPONSE TO RESTRICTION REQUIREMENT

Applicants hereby elect, with traverse, the claims of Group I and the nucleotide sequences of SEQ ID NOs:3, 11, and 15 (which encode SEQ ID NOs:4, 12, and 16) and submit that now pending claims 1-6 and 24-32 are directed to Group I.

In support of the election with traverse, Applicants refer to Example 3 of the application as filed (page 20, line 26 to page 23, line 14); the nucleotide sequences shown in SEQ ID NO:3 and SEQ ID NO:11 are portions of the nucleotide sequence shown in SEQ ID NO:15. Based on the Clustal method of alignment the polypeptides shown in SEQ ID NO:4 and SEQ ID NO:12 are 100% identical to SEQ ID NO:16. See below Table A, which shows the percent identity determined using the Clustal alignment method for all the polypeptides in the application.

TABLE A

Percent Identities of the Amino Acid Sequences of the Present Application

SEQ ID NO:	2	4	6	8	10	12	14	16	17
2	***	15.3	13.6	47.5	49.2	47.5	16.9	47.5	45.8
4	15.3	***	13.3	16.7	41.7	100.0	15.5	100.0	47.6
6	13.6	13.3	***	90.0	46.7	86.7	98.3	86.7	40.0
8	47.5	16.7	90.0	***	47.7	85.2	82.4	86.5	40.3
10	49.2	41.7	46.7	47.7	***	43.3	38.9	38.3	42.1
12	47.5	100.0	86.7	85.2	43.3	***	84.5	100.0	39.1
14	16.9	15.5	98.3	82.4	38.9	84.5	***	84.5	33.7
16	47.5	100.0	86.7	86.5	38.3	100.0	84.5	***	34.1
17	45.8	47.6	40.0	40.3	42.1	39.1	33.7	34.1	***

Please charge any requisite fee or credit any overpayment to Deposit Account No. 04-1928 (E. I. du Pont de Nemours and Company).

In view of the foregoing, a favorable examination of the application on its merits is earnestly solicited.

Applicants' undersigned may be reached at the below-listed numbers.

Respectfully submitted,

J. KENNETH JOUNG
Attorney for Applicants
Reg. No. 41, 881
(302) 992-4929 (phone)
(302) 892-1026 (fax)

Date:

MARKED-UP VERSION SHOWING CHANGES MADE

In showing changes made below, deletions are shown in strikethrough and additions are shown as underlined.

IN THE SPECIFICATION:

Paragraph at page 1, lines 3-5:

This application ~~claims the benefit~~is a continuation in part of International Application No. PCT/US99/25953, filed November 4, 1999, which claims priority of U.S. Provisional Application No. 60/107,242, filed November 5, 1998.

Table 2 on page 17:

TABLE 2

cDNA Libraries from Corn, Rice, and Wheat

~~Li~~ ~~brary~~ Library	Tissue	Clone
~~ed~~ ~~t1c~~ cdt1c	Corn Developing Tassel	~~cdt1c.pk001.l6~~ cdt1c.pk001.l6
~~p0~~ ~~006~~ p0006	Corn Young Shoot	~~p0006.cbyvc82rx~~ p0006.cbyvc82rx
~~rl~~ ~~0n~~ rl0n	Rice 15 Day Old Leaf*	~~rl0n.pk0063.d10~~ rl0n.pk0063.d10
~~rr~~ ~~1~~ rr1	Rice Root of Two Week Old Developing Seedling	~~rr1.pk0001.a11~~ rr1.pk0001.a11
~~w~~ ~~re1n~~ wre1n	Wheat Root From 7 Day Old Etiolated Seedling*	~~wre1n.pk0122.c2~~ wre1n.pk0122.c2

* These libraries were normalized essentially as described in U.S. Patent No. 5,482,845, incorporated herein by reference.

Table 3 on page 21:

TABLE 3

BLAST Results for Clones Encoding Polypeptides Homologous to NPR1

Clone	Status	SEQ ID NO:	BLAST pLog Score NCBI GI No. 1773295
~~cdt1c.pk00~~ ~~1.l6~~ cdt1c.pk001.l6	EST	2	13.22
~~rr1.pk0001.~~ ~~a11~~ cdt1c.pk001.l6	EST	4	32.30
~~wre1n.pk01~~ ~~22.e2~~ cdt1c.pk001.l6	EST	6	15.00

Table 4 on page 21:

TABLE 4

BLAST Results for Sequences Encoding Polypeptides Homologous to NPR1

Clone	~~Stat~~ ~~us~~ Status	SEQ ID NO:	BLAST pLog Score 1773295
~~p0006.cbyvc~~ ~~82rx~~ p0006.cbyvc82rx	FIS	8	60.22
~~rl0n.pk0063.~~ ~~d10:fis~~ rl0n.pk0063.d10:fis	~~CG~~ ~~S~~ CGS	10	138.00
~~rr1.pk0001.a~~ ~~11:fis~~ rr1.pk0001.a11.fis	FIS	12	91.22
~~wre1n.pk012~~ ~~2.e2:fis~~ wre1n.pk0122.c2:fis	FIS	14	22.52

Table 5 on page 22:

TABLE 5

BLAST Results for Sequences Encoding Polypeptides Homologous to NPR1

Clone	Status	SEQ ID NO:	BLAST pLog Score
~~rr1.pk0001.a11:cgs~~ rr1.pk0001.a11:cgs	CGS	16	1773295 100.00

Table 6 on page 22:

TABLE 6

Percent Identity of Amino Acid Sequences Deduced From the Nucleotide Sequences of cDNA Clones Encoding Polypeptides Homologous to NPR1

Clone	SEQ ID NO:	Percent Identity to 1773295
~~cdt1c.pk001.l6~~ cdt1c.pk001.l6	2	45.8
~~rr1.pk0001.a11~~ rr1.pk0001.a11	4	47.6
~~wre1n.pk0122.c2~~ wre1n.pk0122.c2	6	40.0
~~p0006.cbyvc82rx~~ p0006.cbyvc82rx	8	40.3
~~rl0n.pk0063.d10:fis~~ rl0n.pk0063.d10:fis	10	42.1
~~rr1.pk0001.a11:fis~~ rr1.pk0001.a11:fis	12	39.1
~~wre1n.pk0122.c2:fis~~ wre1n.pk0122.c2:fis	14	33.7
~~rr1.pk0001.a11:cgs~~ rr1.pk0001.a11:cgs	16	34.1

IN THE CLAIMS:

1. (Amended) An isolated polynucleotide comprising: (a) a nucleotide sequence encoding a~~that encodes an NPR1~~ polypeptide having NPR1 activity, wherein the polypeptide has an amino acid ~~a~~ sequence ~~identity~~ of at least 80% sequence identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:~~2, 4~~, ~~6, 8, 10~~, 12, ~~14~~, and 16, or (b) a complement of the nucleotide sequence, wherein the complement and the nucleotide sequence consist of the same number of nucleotides and are 100% complementary.

5. (Amended) The polynucleotide of Claim 1 wherein the polynucleotide encodes a polypeptide selected from the group consisting of SEQ ID NOs:~~2, 4~~, ~~6, 8, 10~~, 12, ~~14~~, and 16.

6. (Amended) The polynucleotide of Claim 1 wherein the polynucleotide comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:~~1, 3~~, ~~5, 7, 9~~, 11, ~~13~~, and 15.

24. (Amended) A recombinant DNA construct ~~chimeric gene~~ comprising the polynucleotide of Claim 1 operably linked to at least one regulatory sequence.

25. (Amended) A method for altering the level of pathogen resistance in a plant, the method comprising the steps of:

(a) transforming a plant cell with the recombinant DNA construct of Claim 24 ~~a chimeric gene containing the polypeptide of Claim 1~~;

(b) culturing the transformed plant cell under conditions suitable for the expression of the polynucleotide ~~chimeric gene~~;

(c) maintaining the plant cell under conditions that are suitable for its development into a plant; and

(d) comparing the level of pathogen resistance of the plant cell containing the polynucleotide ~~of Claim 1~~ and a plant cell not containing the polynucleotide ~~of Claim~~ 1.